



Qy 1 NWGPLV 6  
 Db 465 NWGPLV 470

RESULT 3  
 FWSYGS  
 Glycinin chain A5A4B3 precursor - soybean  
 N: Alternative names: 11s Globulin  
 C: Species: Glycine max (soybean)  
 C: Date: 28-Feb-1986 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
 C: Accession: A91145; A91333; A0348; A25253  
 R: Momma, T.; Negoro, T.; Hirano, H.; Matsumoto, A.; Ueda, K.; Fukazawa, C.;  
 Eur. J. Biochem. 149, 491-496, 1985  
 A: Title: Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a splitting stc  
 A: Reference number: A91145; MUID:85230642; PMID:2988947  
 A: Residues: 1-562 <MOM>  
 A: Cross-references: UNIPROT:PO2958; GB:X02626; NID:918628; PIDN:CAA26478.1; PID:9732706  
 A: Molecule type: mRNA  
 A: Experimental source: cv. Bonmarni  
 A: Note: The authors translated the codon TCA for residue 86 as Leu, GAC for residue 145  
 R: Hirano, H.; Fukazawa, C.; Harada, K.  
 FEBS Lett. 181, 124-128, 1985  
 A: Title: The primary structures of the A4 and A5 subunits are highly homologous to that  
 A: Reference number: A91333  
 A: Residues: 1-562 <MOM>  
 A: Molecule type: protein  
 A: Residues: 24-28, 'F', '30-81, 'L', '83-85, 'L', '87-93, 'V', '95-100, 'I', '102, 'M', '104, 'F', '106-116,  
 A: Experimental source: cv. Bonmarni  
 A: Note: Parts of the A4 chain, including the amino end, were sequenced  
 C: Comment: The source of this protein was cotyledon tissue taken from seeds at the middle  
 C: Comment: The glycinin molecule, the major seed storage protein of soybean, is composed  
 identified.  
 C: Comment: Acidic (A5 and A4) and basic (B3) components of this glycinin subunit are syn  
 sulfide bond, that is thought to be noncovalently associated with the A4 chain.  
 C: Superfamily: glycinin  
 C: Keywords: seed; storage protein  
 F: 1/23/Domain: signal sequence #status predicted <SIG>  
 F: 24-120/Product: glycinin, A5 chain #status experimental <GA5>  
 F: 21-377/Product: glycinin, A4 chain #status predicted <GA4>  
 F: 378-562/Product: glycinin, B3 chain #status predicted <GB3>  
 F: 108-384/Disulfide bonds: #status predicted

Query Match 100.0%; Score 38; DB 1; Length 562;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 NWGPLV 6  
 Db 543 NWGPLV 548

RESULT 5  
 Glycinin A5A4B3 chain - soybean  
 C: Species: Glycine max (soybean)  
 C: Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
 C: Accession: S54802  
 R: Xue, Z.  
 A: Residues: 1-563 <XUE>  
 A: Cross-references: UNIPROT:O319921; EMBL:X86970; NID:9806555; PIDN:CAA60533.1; PID:9806555  
 C: Superfamily: glycinin

Query Match 100.0%; Score 38; DB 2; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 NWGPLV 6  
 Db 544 NWGPLV 549

RESULT 6  
 colicin A - Escherichia coli (fragments)  
 C: Species: Escherichia coli  
 C: Date: 31-May-1996 #sequence\_revision 25-Oct-1996 #text\_change 09-Jul-2004  
 C: Accession: I53544; I41169  
 R: Gelli, V.; Liobues, R.; Zaai, S.A.; van Spaendonk, R.M.; Rollin, C.; Benedetti, H.; La  
 FEMS Microbiol. Lett. 109, 335-342, 1993  
 A: Title: Recognition of the colicin A N-terminal epitope 1C11 in vitro and in vivo in Es  
 A: Reference number: I53544; MUID:787969  
 A: Accession: I53544  
 A: Status: preliminary; translated from GB/EMBL/DDJB  
 A: Molecule type: DNA  
 A: Residues: 1-19 <RES>  
 A: Cross-references: UNIPROT:Q47108; EMBL:X73248; NID:9312557  
 R: Baty, D.; Knibbeler, M.; Verheij, H.; Pateus, F.; Shire, D.; Bernadac, A.; Lazdunski, C.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 1152-1156, 1987  
 A: Title: Site-directed mutagenesis of the COOH-terminal region of colicin A: Effect on c  
 A: Reference number: I41169  
 A: Accession: I41169  
 A: Status: preliminary; translated from GB/EMBL/DDJB  
 A: Molecule type: DNA  
 A: Residues: 20-223 <RES2>  
 A: Cross-references: GB:MI15691; NID:9145562; PIDN:AAA23592.1; PMID:2434951  
 C: Superfamily: colicin IB  
 C: Keywords: bacteriocin

Query Match 92.1%; Score 35; DB 2; Length 223;  
 Best Local Similarity 83.3%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 NWGPLV 6  
 Db 148 NWGPLM 153

RESULT 4  
 Glycinin Gy4 precursor - soybean (cv. Forrest)  
 C: Species: Glycine max (soybean)  
 C: Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
 C: Accession: S20946  
 R: Xue, Z.T.; Xu, M.L.; Shen, W.; Zhuang, N.L.; Hu, W.M.; Shen, S.C.  
 Plant Mol. Biol. 18, 89-908, 1992  
 A: Title: Characterization of a Gy4 Glycinin gene from soybean Glycine max cv. Forrest.  
 A: Reference number: S20946; MUID:32256811; PMID:1316192  
 A: Molecule type: DNA  
 A: Residues: 1-562 <XUE>  
 A: Cross-references: UNIPROT:Q43452; EMBL:X52863; NID:918640; PIDN:CAA37044.1; PID:918641  
 A: Experimental source: cv. Forrest  
 C: Genetics:  
 A: Gene: Gy4  
 A: Introns: 97/1; 184/3; 433/3  
 C: Superfamily: glycinin

RESULT 7

SG0867 colicin N - *Escherichia coli* plasmid pCHAP4

C;Species: *Escherichia coli*

C;Accession: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

A;Accession: SG0867

R;Puglley, A.P.

Mol. Microbiol. 1, 317-325, 1987

A;Title: Nucleotide sequencing of the structural gene for colicin N reveals homology between colicin N and colicin M

A;Reference number: SG0867; MUID:88201670; PMID:2834623

A;Accession: S00867

A;Molecule type: DNA

A;Residues: 1-387 <PUG>

A;Cross-references: UNIPROT:PO8083; EMBL:Y00533; NID:941115; PIDN:CAA68592.1; PID:941116

C;Genetics:

A;Gene: cna

A;Genome: plasmid

C;Keywords: bacteriocin; transmembrane protein

Query Match 92.1%; Score 35; DB 2; Length 387;

Best Local Similarity 83.3%; Pred. No. 54;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6

Db 313 NWGPLL 318

RESULT 8

IEUCBB colicin B - *Escherichia coli* plasmid ColBM-pF166

C;Species: *Escherichia coli*

C;Accession: A27089 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004

R;Schramm, E.; Mende, J.; Braun, V.; Kamp, R.M.

J. Bacteriol. 169, 3350-3357, 1987

A;Title: Nucleotide sequence of the colicin B activity gene cba: consensus pentapeptide

A;Accession number: A27089; MUID:87250309; PMID:243391

A;Accession: A27089

A;Molecule type: DNA

A;Residues: 1-511 <SCH>

A;Cross-references: UNIPROT:PO5819; GB:MI6816; PIDN:AAA98063.1; PID:9145567

C;Comment: Colicins are plasmid-encoded proteins that kill sensitive strains of *E. coli* cytoplasmic membrane, leading to dissipation of cellular energy.

C;Genetics:

A;Gene: cba

A;Genome: plasmid

C;Superfamily: colicin IB

C;Keywords: antibiotic; bacteriocin; toxin; transmembrane protein

Query Match 92.1%; Score 35; DB 1; Length 511;

Best Local Similarity 83.3%; Pred. No. 72;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6

Db 439 NWGPLM 444

RESULT 9

KEBCA colicin A - *Citrobacter freundii* (strain CA31) plasmid ColA

C;Species: *Citrobacter freundii*

C;Accession: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004

R;Morlon, J.; Chartier, M.; Baud, M.; Lazdunski, C.

Mol. Gen. Genet. 211, 241-243, 1988

A;Title: The complete nucleotide sequence of the colicinogenic plasmid ColA. High extent of colicinogenicity of ColA

A;Reference number: 140778; MUID:88174422; PMID:2832701

A;Accession: 140784

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-592 <RES>

A;Cross-references: UNIPROT:PO4480; GB:M37402; NID:9144661; PIDN:AAA72879.1; PID:9144661

A;Experimental source: plasmid ColA

R;Morlon, J.; Lioube, R.; Chartier, M.; Lazdunski, C.

J. Mol. Biol. 170, 271-285, 1983

A;Title: Complete nucleotide sequence of the structural gene for colicin A, a gene transcribed by ColA

A;Reference number: A03504; MUID:6313941

A;Accession: A03504

A;Molecule type: DNA

A;Residues: 1-592 <MOR>

A;Cross-references: GB:X01008; GB:X00034; NID:940459; PIDN:CAA25503.1; PID:940460

R;Morlon, J.; Lioube, R.; Chartier, M.; Bonicel, J.; Lazdunski, C.

EMBO J. 2, 787-789, 1983

A;Title: Nucleotide sequence of promoter, operator and amino-terminal region of colicin A

A;Reference number: 140777; MUID:8405775; PMID:6641715

A;Accession: I40777

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-53 'X' 55-70 <RE2>

A;Cross-references: GB:M26169; NID:9144659; PIDN:AAA98057.1; PID:9144650

A;Experimental source: Plasmid ColA

C;Comment: This protein acts to depolarize the bacterial inner membrane, most likely by forming pores in the membrane

C;Genetics:

A;Gene: caa

A;Genome: plasmid

C;Superfamily: colicin IB

C;Keywords: antibiotic; bacteriocin; toxin; transmembrane protein

C;Keywords: colicin

Qy 1 NWGPLV 6

Db 517 NWGPLM 522

RESULT 10

EB4708 probable signal peptidase I (imported) - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Accession: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; vanAken, S.B.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Accession number: A84420; MUID:20083487; PMID:10617197

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-250 <STO>

A;Cross-references: UNIPROT:004348; GB:AB002093; NID:91946373; PIDN:AA863091.1; GSPDB:G

C;Genetics:

A;Gene: At2g30440

A;Accession: EB4708

A;Map position: 2

Query Match 89.5%; Score 34; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPL 5

Db 209 NWGPL 213

RESULT 11

F84071 hypothetical protein BII3374 (imported) - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Accession: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C;Accession: F84071

R; Takami, H.; Nakasone, K.; Takasaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirai Nucleic Acids Res. 28, 4317-4331, 2000  
 A; Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and  
 A; Reference number: A83650; MUID:20512582; PMID:11058132  
 A; Accession: F84071  
 A; Status: Preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-265 <STO>  
 A; Cross-references: UNIPROT:Q93717; GB:AP001518; NID:910175792; PIDN:BA0700  
 C; Experimental source: strain C-125  
 A; Gene: BH3374

RESULT 12  
 Query Match 89.5%; Score 34; DB 2; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 NWGPL 5  
 Db 172 NWGPL 176

RESULT 13  
 Query Match 89.5%; Score 34; DB 2; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 NWGPL 5  
 Db 326 NWGPL 330

RESULT 14  
 Query Match 89.5%; Score 34; DB 2; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 1e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 NWGPL 5  
 Db 45 NWGPL 49

RESULT 15  
 T50435  
 Conserved hypothetical protein SPCC4B3.13 [imported] - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T50435  
 R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, November 1999  
 A;Reference number: Z25033  
 A;Accession: T50435  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-539 <SEE>  
 A;Cross-references: UNIPROT:Q9USK3; EMBL:AL132870; PIDN:CA860687.1; GSPDB:GN00068; SPDB: B86203  
 probable signal peptidase [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: E86203  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Arnes, N.F.; Hughes, B.; L.; Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, C.; Maiti, R.; Marzali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: E86203  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-367 <STO>  
 A;Cross-references: UNIPROT:Q9M9Z2; GB:AE005172; NID:97523697; PIDN:AAF63136.1; GSPDB:GN  
 C;Genetics:  
 A;Map position: 1

RESULT 15  
 D70413  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoD2 [similarity] - *Aquifex aeolicus*.  
 C;Species: *Aquifex aeolicus*  
 C;Accession: D70413  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 12-Jul-2004  
 C;Accession: D70413  
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: D70413  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-566 <QFQ>  
 A;Cross-references: UNIPROT:O67335; GB:AE000734; NID:92983733; PIDN:AAC07298.1; PID:9298  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: nuoD2  
 C;Superfamily: [NiFe]-hydrogenase-3-type complex, fused large subunit/NADH:quinone oxidoreductase  
 C;Keywords: NAD; oxidoreductase

RESULT 16  
 PS0154  
 12S surface antigen M17 - *Entamoeba histolytica* (fragment)  
 C;Species: *Entamoeba histolytica*  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C;Accession: PS0154  
 R;Edman, U.; Meraz, M.A.; Rausser, S.; Agabian, N.; Meza, I.  
 J. Exp. Med. 172, 879-888, 1990  
 A;Title: Characterization of an immuno-dominant variable surface antigen from pathogenic  
 A;Reference number: JH0284; MUID:903354789; PMID:1693956  
 A;Accession: PS0154  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-471 <EDM>  
 A;Cross-references: UNIPROT:Q05351  
 A;Experimental source: strain REP291

Search completed: November 6, 2004, 19:54:13  
 Job time : 15.625 secs